



Supplementary Figure 9. Clustering of sRNA-seq samples. We used NMDS, PCC (Figure 3), MDS (A and B), and PCA (C and D) to estimate sample differences and similarities. Each data point represents the collapsed miRNA expression data from one sample. Blue, epiphytic fungal mycelium (MYC); green, infected epidermis without mycelium (EPI); light blue, fungal haustoria (HAU); purple, microsomes of the epidermis without haustoria (P40); orange, apoplastic extracellular vesicles (EV+); grey, apoplastic extracellular vesicles of non-infected control plants (EV-).